RAW SEQUENCE LISTING
ERROR REPORT

AUG 2 2 2003

--~/I ~cNTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information
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Application Serial Number: _08/657,749C_

Source: _1600_

Date Processed by STIC: _8/18/2003_

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
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Revised 04/24/2003

1600

```
            RAW SEQUENCE LISTING               DATE: 08/18/2003
            PATENT APPLICATION:  US/08/657,749C     TIME: 13:10:45

            Input Set : A:\1651802.app
            Output Set: N:\CRF4\08182003\H657749C.raw

 3  <110> APPLICANT: METZ, JAMES G.
 4         LARDIZABAL, KATHRYN D.
 5         LASSNER, MICHAEL
 7  <120> TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING A PLANT CYTOPLASMIC
 8         PROTEIN INVOLVED IN FATTY ACYL-COA METABOLISM
10  <130> FILE REFERENCE: 16518.025
12  <140> CURRENT APPLICATION NUMBER: 08/657,749C
13  <141> CURRENT FILING DATE: 1996-05-30
15  <150> PRIOR APPLICATION NUMBER: PCT/US94/13686
16  <151> PRIOR FILING DATE: 1994-11-30
18  <150> PRIOR APPLICATION NUMBER: 08/265,047
19  <151> PRIOR FILING DATE: 1994-06-23
21  <150> PRIOR APPLICATION NUMBER: 08/160,602
22  <151> PRIOR FILING DATE: 1993-11-30
24  <150> PRIOR APPLICATION NUMBER: 08/066,299
25  <151> PRIOR FILING DATE: 1993-05-20
27  <150> PRIOR APPLICATION NUMBER: PCT/US92/09863
28  <151> PRIOR FILING DATE: 1992-11-13
30  <150> PRIOR APPLICATION NUMBER: 07/933,411
31  <151> PRIOR FILING DATE: 1992-08-21
33  <150> PRIOR APPLICATION NUMBER: 07/796,256
34  <151> PRIOR FILING DATE: 1991-11-20
36  <160> NUMBER OF SEQ ID NOS: 53
38  <170> SOFTWARE: PatentIn Ver. 2.1
40  <210> SEQ ID NO: 1
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42  <212> TYPE: DNA
43  <213> ORGANISM: Simmondsia chinensis
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46  <221> NAME/KEY: CDS
47  <222> LOCATION: (80)..(1558)
49  <220> FEATURE:
50  <221> NAME/KEY: modified_base
51  <222> LOCATION: (1537)
52  <223> OTHER INFORMATION: a, c, t, or g
54  <220> FEATURE:
55  <221> NAME/KEY: modified_base
56  <222> LOCATION: (1608)..(1609)
57  <223> OTHER INFORMATION: a, c, t, or g
59  <400> SEQUENCE: 1
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62  gtagcaaact taaaagaaa atg gag gaa atg gga agc att tta gag ttt ctt  112
63                      Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu
```

Doos Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 08/18/2003
PATENT APPLICATION: US/08/657,749C   TIME: 13:10:45

Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

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64                      1            5                10
66 gat aac aaa gcc att ttg gtc act ggt gct act ggc tcc tta gca aaa    160
67 Asp Asn Lys Ala Ile Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys
68              15              20                  25
70 att ttt gtg gag aag gta ctg agg agt caa ccg aat gtg aag aaa ctc    208
71 Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu
72          30                  35                  40
74 tat ctt ctt ttg aga gca acc gat gac gag aca gct gct cta cgc ttg    256
75 Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu
76      45                  50                  55
78 caa aat gag gtt ttt gga aaa gag ttg ttc aaa gtt ctg aaa caa aat    304
79 Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn
80   60                  65                  70                  75
82 tta ggt gca aat ttc tat tcc ttt gta tca gaa aaa gtg act gta gta    352
83 Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val
84                  80                  85                  90
86 ccc ggt gat att act ggt gaa gac ttg tgt ctc aaa gac gtc aat ttg    400
87 Pro Gly Asp Ile Thr Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu
88              95              100                 105
90 aag gaa gaa atg tgg agg gaa atc gat gtt gtt gtc aat cta gct gct    448
91 Lys Glu Glu Met Trp Arg Glu Ile Asp Val Val Val Asn Leu Ala Ala
92          110                 115                 120
94 aca atc aac ttc att gaa agg tac gac gtg tct ctg ctt atc aac aca    496
95 Thr Ile Asn Phe Ile Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr
96      125                 130                 135
98 tat gga gcc aag tat gtt ttg gac ttc gcg aag aag tgc aac aaa tta    544
99 Tyr Gly Ala Lys Tyr Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu
100 140                 145                 150                 155
102 aag ata ttt gtt cat gta tct act gct tat gta tct gga gag aaa aat    592
103 Lys Ile Phe Val His Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn
104             160                 165                 170
106 ggg tta ata ctg gag aag cct tat tat atg ggc gag tca ctt aat gga    640
107 Gly Leu Ile Leu Glu Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly
108         175                 180                 185
110 aga tta ggt ctg gac att aat gta gag aag aaa ctt gtg gag gca aaa    688
111 Arg Leu Gly Leu Asp Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys
112         190                 195                 200
114 atc aat gaa ctt caa gca gcg ggg gca acg gaa aag tcc att aaa tcg    736
115 Ile Asn Glu Leu Gln Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser
116     205                 210                 215
118 aca atg aag gac atg ggc atc gag agg gca aga cac tgg gga tgg cca    784
119 Thr Met Lys Asp Met Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro
120 220                 225                 230                 235
122 aat gtg tat gta ttc acc aag gca tta ggg gag atg ctt ttg atg caa    832
123 Asn Val Tyr Val Phe Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln
124             240                 245                 250
126 tac aaa ggg gac att ccg ctt act att att cgt ccc acc atc atc acc    880
127 Tyr Lys Gly Asp Ile Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr
128         255                 260                 265
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RAW SEQUENCE LISTING   DATE: 08/18/2003
PATENT APPLICATION: US/08/657,749C   TIME: 13:10:45

Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

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130 agc act ttt aaa gag ccc ttt cct ggt tgg gtt gaa ggt gtc agg acc   928
131 Ser Thr Phe Lys Glu Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr
132         270                 275                 280
134 atc gat aat gta cct gta tat tat ggt aaa ggg aga ttg agg tgt atg   976
135 Ile Asp Asn Val Pro Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met
136     285                 290                 295
138 ctt tgc gga ccc agc aca ata att gac ctg ata ccg gca gat atg gtc  1024
139 Leu Cys Gly Pro Ser Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val
140 300                 305                 310                 315
142 gtg aat gca acg ata gta gcc atg gtg gcg cac gca aac caa aga tac  1072
143 Val Asn Ala Thr Ile Val Ala Met Val Ala His Ala Asn Gln Arg Tyr
144             320                 325                 330
146 gta gag ccg gtg aca tac cat gtg gga tct tca gcg gcg aat cca atg  1120
147 Val Glu Pro Val Thr Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met
148             335                 340                 345
150 aaa ctg agt gca tta cca gag atg gca cac cgt tac ttc acc aag aat  1168
151 Lys Leu Ser Ala Leu Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn
152         350                 355                 360
154 cca tgg atc aac ccg gat cgc aac cca gta cat gtg ggt cgg gct atg  1216
155 Pro Trp Ile Asn Pro Asp Arg Asn Pro Val His Val Gly Arg Ala Met
156     365                 370                 375
158 gtc ttc tcc tcc ttc tcc acc ttc cac ctt tat ctc acc ctt aat ttc  1264
159 Val Phe Ser Ser Phe Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe
160 380                 385                 390                 395
162 ctc ctt cct ttg aag gta ctg gag ata gca aat aca ata ttc tgc caa  1312
163 Leu Leu Pro Leu Lys Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln
164             400                 405                 .410
166 tgg ttc aag ggt aag tac atg gat ctt aaa agg aag acg agg ttg ttg  1360
167 Trp Phe Lys Gly Lys Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu
168             415                 420                 425
170 ttg cgt tta gta gac att tat aaa ccc tac ctc ttc ttc caa ggc atc  1408
171 Leu Arg Leu Val Asp Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile
172         430                 435                 440
174 ttt gat gac atg aac act gag aag ttg cgg att gct gca aaa gaa agc  1456
175 Phe Asp Asp Met Asn Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser
176     445                 450                 455
178 ata gtt gaa gct gat atg ttt tac ttt gat ccc agg gca att aac tgg  1504
179 Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp
180 460                 465                 470                 475
W--> 182 gaa gat tac ttc ttg aaa act cat ttc cca ggn gtc gta gag cac gtt  1552
183 Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val
184             480                 485                 490
186 ctt aac taaaagttac ggtacgaaaa tgagaagatt ggaatgcatg caccgaaagn  1608
187 Leu Asn
189 ncaacataaa agacgtggtt aaagtcatgg tcaaaaaga aataaaatgc agttaggttt  1668
191 gtgttgcagt tttgattcct tgtattgtta cttgtacttt tgatctttt cttttttaat 1728
193 gaaatttctc tctttgtttt gtgaaaaaaa aaaaaaaaaa gagctcctgc agaagctt   1786
196 <210> SEQ ID NO: 2
197 <211> LENGTH: 493
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198 <212> TYPE: PRT
199 <213> ORGANISM: Simmondsia chinensis
201 <400> SEQUENCE: 2
202 Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu Asp Asn Lys Ala Ile
203    1               5                  10                  15
205 Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys Ile Phe Val Glu Lys
206            20                  25                  30
208 Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu Tyr Leu Leu Leu Arg
209            35                  40                  45
211 Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu Gln Asn Glu Val Phe
212        50                  55                  60
214 Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn Leu Gly Ala Asn Phe
215  65                  70                  75                  80
217 Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val Pro Gly Asp Ile Thr
218                85                  90                  95
220 Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu Lys Glu Glu Met Trp
221            100                 105                 110
223 Arg Glu Ile Asp Val Val Val Asn Leu Ala Ala Thr Ile Asn Phe Ile
224            115                 120                 125
226 Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr Tyr Gly Ala Lys Tyr
227        130                 135                 140
229 Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu Lys Ile Phe Val His
230 145                 150                 155                 160
232 Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn Gly Leu Ile Leu Glu
233                165                 170                 175
235 Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly Arg Leu Gly Leu Asp
236            180                 185                 190
238 Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys Ile Asn Glu Leu Gln
239            195                 200                 205
241 Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser Thr Met Lys Asp Met
242        210                 215                 220
244 Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro Asn Val Tyr Val Phe
245 225                 230                 235                 240
247 Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln Tyr Lys Gly Asp Ile
248            245                 250                 255
250 Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr Ser Thr Phe Lys Glu
251            260                 265                 270
253 Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr Ile Asp Asn Val Pro
254            275                 280                 285
256 Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met Leu Cys Gly Pro Ser
257        290                 295                 300
259 Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val Val Asn Ala Thr Ile
260 305                 310                 315                 320
262 Val Ala Met Val Ala His Ala Asn Gln Arg Tyr Val Glu Pro Val Thr
263            325                 330                 335
265 Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met Lys Leu Ser Ala Leu
266            340                 345                 350
268 Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn Pro Trp Ile Asn Pro
269        355                 360                 365
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RAW SEQUENCE LISTING   DATE: 08/18/2003
PATENT APPLICATION: US/08/657,749C   TIME: 13:10:45

Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

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271 Asp Arg Asn Pro Val His Val Gly Arg Ala Met Val Phe Ser Ser Phe
272     370             375             380
274 Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe Leu Leu Pro Leu Lys
275 385             390             395             400
277 Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln Trp Phe Lys Gly Lys
278             405             410             415
280 Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu Leu Arg Leu Val Asp
281             420             425             430
283 Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile Phe Asp Asp Met Asn
284             435             440             445
286 Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser Ile Val Glu Ala Asp
287     450             455             460
289 Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp Glu Asp Tyr Phe Leu
290 465             470             475             480
292 Lys Thr His Phe Pro Gly Val Val Glu His Val Leu Asn
293             485             490
297 <210> SEQ ID NO: 3
298 <211> LENGTH: 1733
299 <212> TYPE: DNA
300 <213> ORGANISM: Simmondsia chinensis
302 <220> FEATURE:
303 <221> NAME/KEY: CDS
304 <222> LOCATION: (39)..(1610)
306 <220> FEATURE:
307 <221> NAME/KEY: modified_base
308 <222> LOCATION: (676)
309 <223> OTHER INFORMATION: a, c, t, or g
311 <400> SEQUENCE: 3
312 ggaactccat cccttcctcc ctcactcctc tctctaca atg aag gcc aaa aca atc 56
313                                            Met Lys Ala Lys Thr Ile
314                                             1               5
316 aca aac ccg gag atc caa gtc tcc acg acc atg acc acc acg acc acg 104
317 Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr
318             10              15              20
320 act atg acc gcc act ctc ccc aac ttc aag tcc tcc atc aac tta cac 152
321 Thr Met Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser Ile Asn Leu His
322         25              30              35
324 cac gtc aag ctc ggc tac cac tac tta atc tcc aat gcc ctc ttc ctc 200
325 His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu
326     40              45              50
328 gta ttc atc ccc ctt ttg ggc ctc gct tcg gcc cat ctc tcc tcc ttc 248
329 Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His Leu Ser Ser Phe
330 55              60              65              70
332 tcg gcc cat gac ttg tcc ctg ctc ttc gac ctc ctt cgc cgc aac ctc 296
333 Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu Arg Arg Asn Leu
334             75              80              85
336 ctc cct gtt gtc gtt tgt tct ttc ctc ttc gtt tta tta gca acc cta 344
337 Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu Leu Ala Thr Leu
338             90              95              100
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08/657,749 6

```
        agc ttg ttt aac cca acg ccg tcg ctg tca tcc atg ata gtt aac cat    728
        Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His
"n"     215                 220                 225                 230
        tac aag ctn agg ggt aat ata ctt agc tat aat ctt ggt ggc atg ggt    776
location Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly
                            235                 240                 245
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see p. 7 for more errors

<210> SEQ ID NO 4
<211> LENGTH: 524
<212> TYPE: PRT
<213> ORGANISM: Simmondsia chinensis
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (213)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 4

what about Xaa at location 233?

see below

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1               5                   10                  15
Met Thr Thr Thr Thr Thr Thr Met Thr Ala Thr Leu Pro Asn Phe Lys
            20                  25                  30
Ser Ser Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile
        35                  40                  45
Ser Asn Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser
    50                  55                  60
Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp
65              70                  75                      80
Leu Leu Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe
            85                  90                  95
Val Leu Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr
        100                 105                 110
Leu Val Asp Phe Gly Cys Tyr Lys Pro Gln Pro Asn Leu Met Thr Ser
        115                 120                 125
His Glu Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys
    130                 135                 140
Glu Asn Ile Glu Phe Gln Arg Lys Ile Leu Glu Arg Ala Gly Met Gly
145                 150                 155                 160
Arg Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Ala Glu Pro
            165                 170                 175
Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala
        180                 185                 190
Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly
        195                 200                 205
Ile Leu Val Val Xaa Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser
        210                 215                 220
Ser Met Ile Val Asn His Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr
225                 230                 235                 240
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/18/2003
PATENT APPLICATION: US/08/657,749C TIME: 13:10:46

Input Set : A:\1651802.app
Output Set: N:\CRF4\08182003\H657749C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1537,1608,1609
Seq#:3; N Pos. 676,737
Seq#:3; Xaa Pos. 213,233
Seq#:4; Xaa Pos. 213,233
Seq#:22; N Pos. 345
Seq#:22; Xaa Pos. 102
Seq#:23; Xaa Pos. 102
Seq#:24; N Pos. 155,217
Seq#:24; Xaa Pos. 51,72
Seq#:25; Xaa Pos. 51,72
Seq#:31; Xaa Pos. 3,10
Seq#:35; Xaa Pos. 4,5
Seq#:36; Xaa Pos. 7,8,11
Seq#:38; Xaa Pos. 1,17
Seq#:39; Xaa Pos. 7
Seq#:42; N Pos. 9,12,15
Seq#:43; N Pos. 15
Seq#:46; Xaa Pos. 3
Seq#:47; N Pos. 30,33
Seq#:49; N Pos. 30,33,36
Seq#:50; N Pos. 29,32,35
Seq#:52; N Pos. 39
Seq#:53; N Pos. 27

Please ensure these n/Xaa locations are explained